Full wwPDB X-ray Structure Validation Report (i)

Oct 31, 2023 – 02:42 PM JST

PDB ID	:	5GIV
Title	:	Crystal structure of M32 carboxypeptidase from Deinococcus radiodurans R1
Authors	:	Sharma, B.; Singh, R.; Yadav, P.; Ghosh, B.; Kumar, A.; Jamdar, S.N.; Makde, R.D.
Deposited on	:	2016-06-25
Resolution	:	2.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

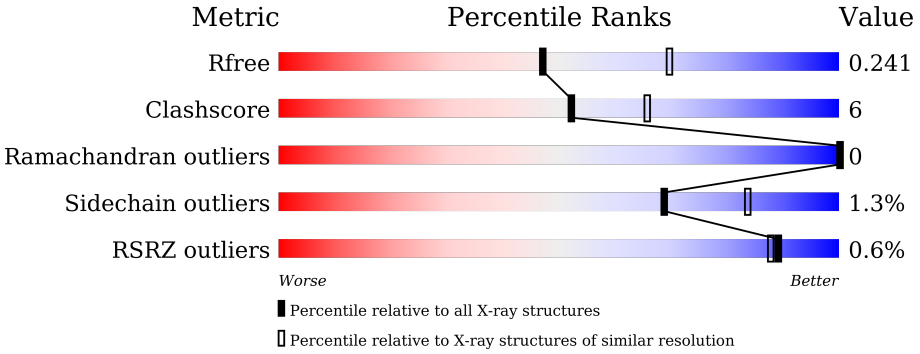
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	503	89% 10% •
1	B	503	88% 11%
1	C	503	87% 12% •
1	D	503	% 89% 9% •
1	E	503	% 83% 16% •
1	F	503	% 85% 15%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 24483 atoms, of which 3 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

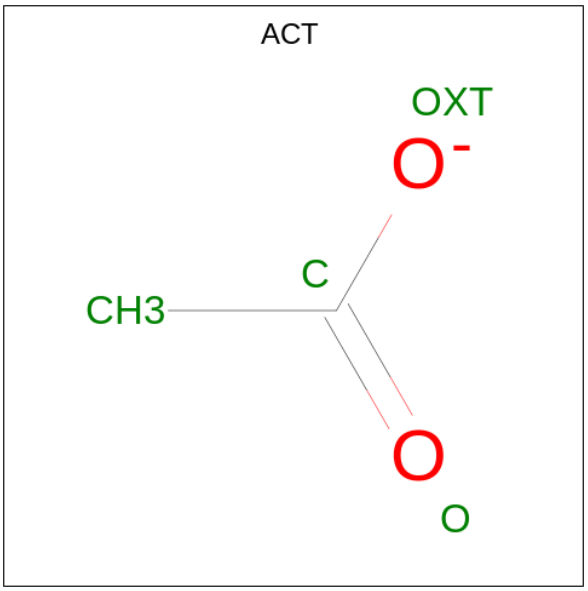
- Molecule 1 is a protein called Carboxypeptidase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	497	3908	2464	700	738	6	0	0	0
1	B	501	3958	2492	709	751	6	0	1	0
1	C	495	3916	2468	703	739	6	0	0	0
1	D	497	3922	2471	703	742	6	0	0	0
1	E	497	3908	2465	698	739	6	0	0	0
1	F	501	3943	2484	709	744	6	0	0	0

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
2	A	1	1	1	0	0
2	B	1	1	1	0	0
2	C	1	1	1	0	0
2	D	1	1	1	0	0
2	E	1	1	1	0	0
2	F	1	1	1	0	0

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
3	D	1	7	2	3	2	0	0

- Molecule 4 is water.

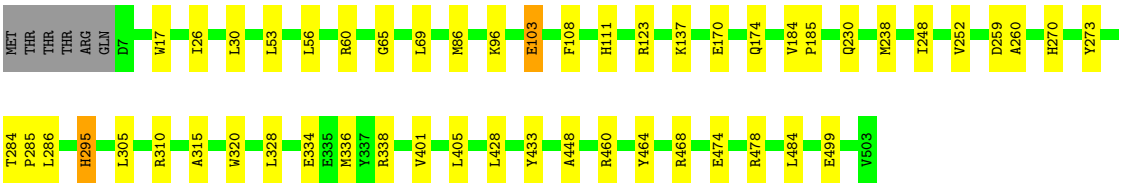
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	175	176	176	0	1
			Total	O		
4	B	196	197	197	0	1
			Total	O		
4	C	158	158	158	0	0
			Total	O		
4	D	192	197	197	0	5
			Total	O		
4	E	93	94	94	0	1
			Total	O		
4	F	93	93	93	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

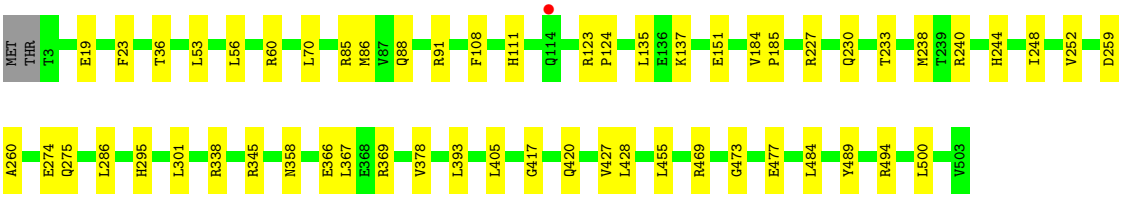
• Molecule 1: Carboxypeptidase 1

Chain A:



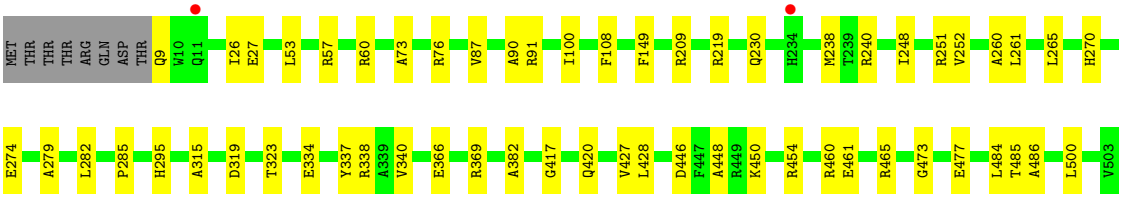
• Molecule 1: Carboxypeptidase 1

Chain B:



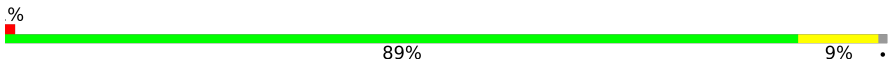
• Molecule 1: Carboxypeptidase 1

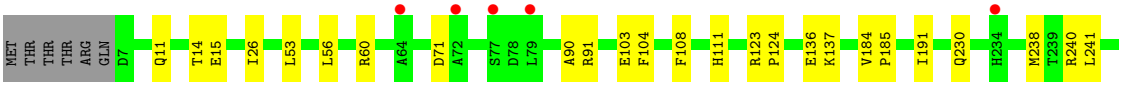
Chain C:

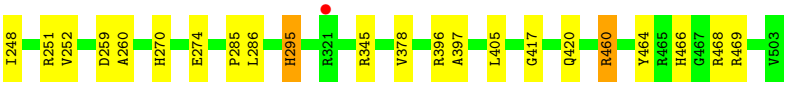


• Molecule 1: Carboxypeptidase 1

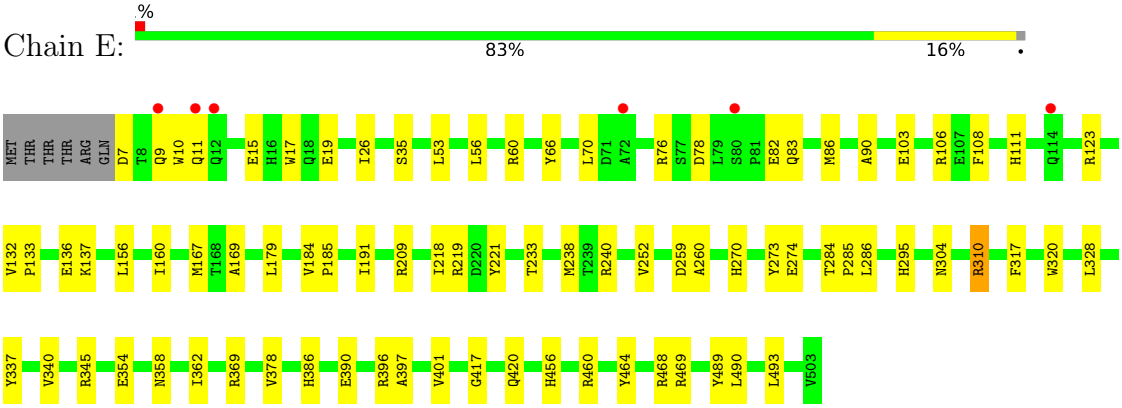
Chain D:



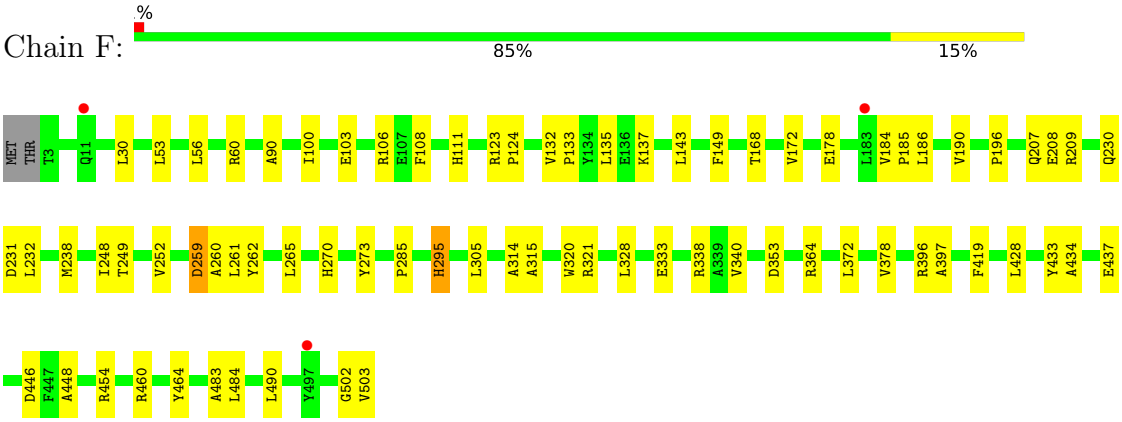




• Molecule 1: Carboxypeptidase 1



• Molecule 1: Carboxypeptidase 1



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	134.86Å 256.63Å 199.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.97 – 2.40 47.97 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.8 (47.97-2.40) 99.9 (47.97-2.40)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.07 (at 2.39Å)	Xtriage
Refinement program	PHENIX (1.10_2152: ???)	Depositor
R, R_{free}	0.205 , 0.243 0.205 , 0.241	Depositor DCC
R_{free} test set	6745 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	27.3	Xtriage
Anisotropy	0.530	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 27.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	24483	wwPDB-VP
Average B, all atoms (Å^2)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 49.51 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 7.3878e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: ACT, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	A	0.34	0/4007	0.49	0/5438
1	B	0.33	0/4060	0.49	0/5508
1	C	0.32	0/4015	0.48	0/5445
1	D	0.33	0/4021	0.48	0/5456
1	E	0.31	0/4007	0.47	0/5439
1	F	0.31	0/4042	0.48	0/5484
All	All	0.32	0/24152	0.48	0/32770

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3908	0	3689	40	0
1	B	3958	0	3745	38	0
1	C	3916	0	3717	36	0
1	D	3922	0	3708	34	0
1	E	3908	0	3688	61	0
1	F	3943	0	3728	51	0
2	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
3	D	4	3	3	1	0
4	A	176	0	0	1	0
4	B	197	0	0	3	0
4	C	158	0	0	4	0
4	D	197	0	0	0	0
4	E	94	0	0	2	0
4	F	93	0	0	3	0
All	All	24480	3	22278	254	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (254) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:17:TRP:CZ3	1:A:86:MET:HE2	2.07	0.89
1:D:136:GLU:HG3	1:D:378:VAL:HG21	1.56	0.86
1:C:446:ASP:OD2	1:C:454:ARG:HD3	1.77	0.83
1:F:103:GLU:OE1	1:F:106:ARG:NH2	2.13	0.80
1:E:17:TRP:CZ3	1:E:86:MET:HE2	2.20	0.77
1:A:328:LEU:HD11	1:A:336:MET:CE	2.15	0.77
1:F:446:ASP:OD2	1:F:454:ARG:HD3	1.87	0.75
1:D:136:GLU:HG3	1:D:378:VAL:CG2	2.17	0.74
1:D:71:ASP:OD1	1:D:91:ARG:NH1	2.22	0.73
1:B:494:ARG:HD3	4:B:809:HOH:O	1.89	0.72
1:A:86:MET:CE	1:A:284:THR:HB	2.20	0.72
1:B:240:ARG:NH1	1:B:274:GLU:OE2	2.23	0.71
1:A:86:MET:HE3	1:A:284:THR:HB	1.72	0.70
1:C:219:ARG:HD2	4:C:731:HOH:O	1.92	0.69
1:A:238:MET:CE	1:A:270:HIS:HB3	2.22	0.69
1:A:103:GLU:HB2	4:A:770:HOH:O	1.91	0.69
1:A:170:GLU:O	1:A:174:GLN:HG3	1.93	0.69
1:C:366:GLU:HG2	1:C:369:ARG:NH2	2.09	0.67
1:E:86:MET:CE	1:E:284:THR:HB	2.24	0.67
1:E:320:TRP:CD1	1:E:328:LEU:HD21	2.29	0.67
1:A:310:ARG:NH2	1:A:499:GLU:OE1	2.27	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:136:GLU:HG3	1:E:378:VAL:HG21	1.76	0.66
1:D:123:ARG:HB3	1:D:124:PRO:HD3	1.77	0.66
1:B:111:HIS:CE1	1:B:137:LYS:HD3	2.31	0.65
1:F:396:ARG:NH1	1:F:397:ALA:O	2.29	0.65
1:B:60:ARG:NH2	1:F:56:LEU:HD21	2.11	0.65
1:E:136:GLU:HG3	1:E:378:VAL:CG2	2.26	0.65
1:E:86:MET:HE1	1:E:284:THR:HB	1.77	0.65
1:E:310:ARG:HD3	1:E:337:TYR:CD2	2.32	0.65
1:C:60:ARG:NH2	1:E:56:LEU:HD21	2.14	0.63
1:E:317:PHE:CE1	1:E:328:LEU:HD23	2.32	0.63
1:D:111:HIS:ND1	1:D:137:LYS:HD3	2.14	0.63
1:E:7:ASP:O	1:E:10:TRP:HB3	1.98	0.63
1:C:100:ILE:HD11	1:C:149:PHE:HE1	1.64	0.63
1:E:396:ARG:NH1	1:E:397:ALA:O	2.33	0.62
1:A:56:LEU:O	1:A:60:ARG:HG2	1.99	0.62
1:C:240:ARG:NH1	1:C:274:GLU:OE1	2.34	0.61
1:B:111:HIS:ND1	1:B:137:LYS:HD3	2.15	0.61
1:E:86:MET:HG2	1:E:286:LEU:HG	1.82	0.61
1:A:238:MET:HE3	1:A:270:HIS:HB3	1.83	0.60
1:C:319:ASP:OD2	1:C:450:LYS:NZ	2.31	0.60
1:E:238:MET:CE	1:E:270:HIS:HB3	2.32	0.60
1:B:230:GLN:HA	1:B:248:ILE:O	2.01	0.59
1:B:428:LEU:HD21	1:B:484:LEU:HD13	1.84	0.59
1:E:320:TRP:HD1	1:E:328:LEU:HD21	1.66	0.59
1:F:123:ARG:HB3	1:F:124:PRO:HD3	1.83	0.59
1:C:334:GLU:OE2	1:C:338:ARG:NH1	2.36	0.59
1:B:123:ARG:HB3	1:B:124:PRO:HD3	1.83	0.59
1:C:230:GLN:HA	1:C:248:ILE:O	2.04	0.58
1:A:238:MET:HE2	1:A:270:HIS:HB3	1.84	0.58
1:C:209:ARG:NH1	1:C:323:THR:O	2.36	0.58
1:F:196:PRO:HB3	1:F:338:ARG:HE	1.69	0.58
1:F:321:ARG:HA	1:F:328:LEU:HD13	1.85	0.58
1:D:111:HIS:CE1	1:D:137:LYS:HB3	2.39	0.58
1:E:238:MET:HE3	1:E:270:HIS:HB3	1.86	0.58
1:E:358:ASN:O	1:E:362:ILE:HG13	2.04	0.57
1:F:259:ASP:HB3	4:F:704:HOH:O	2.04	0.57
1:A:86:MET:HG2	1:A:286:LEU:HG	1.85	0.57
1:B:85:ARG:NE	1:B:469:ARG:O	2.38	0.57
1:D:238:MET:CE	1:D:270:HIS:HB3	2.33	0.57
1:C:461:GLU:OE2	1:C:465:ARG:NH2	2.37	0.56
1:E:179:LEU:HD23	1:E:490:LEU:HD21	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:328:LEU:HD11	1:A:336:MET:HE3	1.89	0.55
1:E:35:SER:O	1:E:233:THR:HG22	2.06	0.55
1:B:345:ARG:HD3	1:B:393:LEU:O	2.06	0.55
1:E:310:ARG:HD3	1:E:337:TYR:CE2	2.42	0.55
1:E:86:MET:HE3	1:E:285:PRO:HD2	1.88	0.55
1:E:386:HIS:O	1:E:390:GLU:HG3	2.08	0.54
1:E:26:ILE:CG2	1:E:53:LEU:HD21	2.38	0.54
1:E:26:ILE:HG22	1:E:53:LEU:HD21	1.88	0.54
1:B:428:LEU:CD2	1:B:484:LEU:HD13	2.38	0.54
1:F:135:LEU:CB	1:F:378:VAL:HG11	2.37	0.54
1:C:27:GLU:OE1	1:C:57:ARG:HD3	2.08	0.54
1:D:136:GLU:CG	1:D:378:VAL:HG21	2.35	0.54
1:D:396:ARG:NH1	1:D:397:ALA:O	2.41	0.54
1:E:82:GLU:OE2	1:E:469:ARG:NH1	2.41	0.54
1:C:87:VAL:O	1:C:91:ARG:HG3	2.07	0.53
1:E:160:ILE:CD1	1:E:169:ALA:HA	2.37	0.53
1:D:238:MET:HE3	1:D:270:HIS:HB3	1.90	0.53
1:B:427:VAL:CG2	1:B:484:LEU:HD11	2.39	0.53
1:D:111:HIS:CE1	1:D:137:LYS:HD3	2.44	0.53
1:E:76:ARG:HH21	1:E:78:ASP:CB	2.21	0.53
1:A:230:GLN:HA	1:A:248:ILE:O	2.09	0.53
1:E:26:ILE:HG22	1:E:53:LEU:CD2	2.39	0.52
1:B:111:HIS:CE1	1:B:137:LYS:HB3	2.45	0.52
1:D:123:ARG:HA	1:D:405:LEU:HD13	1.90	0.52
1:E:240:ARG:NH1	1:E:274:GLU:OE1	2.42	0.52
1:F:207:GLN:NE2	1:F:232:LEU:HD11	2.25	0.52
1:E:10:TRP:CZ2	1:E:83:GLN:HG2	2.44	0.52
1:A:320:TRP:HE1	1:A:336:MET:CE	2.23	0.51
1:C:238:MET:CE	1:C:270:HIS:HB3	2.41	0.51
1:F:262:TYR:OH	1:F:340:VAL:HG11	2.11	0.51
1:A:315:ALA:HB2	1:A:448:ALA:HA	1.93	0.51
1:A:184:VAL:HB	1:A:185:PRO:HD3	1.92	0.51
1:D:238:MET:H	3:D:602:ACT:H2	1.75	0.51
1:D:26:ILE:CG2	1:D:53:LEU:HD11	2.42	0.50
1:F:90:ALA:HB2	1:F:285:PRO:HG2	1.93	0.50
1:C:334:GLU:O	1:C:338:ARG:HG3	2.11	0.50
1:B:135:LEU:HB2	1:B:378:VAL:HG11	1.94	0.50
1:B:427:VAL:HG21	1:B:484:LEU:HD11	1.93	0.50
1:F:135:LEU:HB3	1:F:378:VAL:HG11	1.92	0.50
1:A:123:ARG:HA	1:A:405:LEU:HD13	1.93	0.49
1:A:26:ILE:HG22	1:A:53:LEU:HD11	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:26:ILE:HG22	1:D:53:LEU:HD11	1.95	0.49
1:E:66:TYR:CZ	1:E:70:LEU:HD11	2.47	0.49
1:B:227:ARG:NH2	1:B:275:GLN:O	2.45	0.49
1:C:473:GLY:O	1:C:477:GLU:HG3	2.13	0.49
1:A:111:HIS:ND1	1:A:137:LYS:HD3	2.28	0.49
1:A:26:ILE:CG2	1:A:53:LEU:HD11	2.42	0.48
1:A:86:MET:HE1	1:A:284:THR:HB	1.94	0.48
1:A:305:LEU:HD13	1:A:433:TYR:CB	2.43	0.48
1:D:251:ARG:NH1	1:D:259:ASP:OD2	2.46	0.48
1:C:238:MET:HE2	1:C:270:HIS:HB3	1.94	0.48
1:B:123:ARG:HA	1:B:405:LEU:HD13	1.96	0.48
1:D:230:GLN:HA	1:D:248:ILE:O	2.14	0.48
1:C:251:ARG:O	1:C:251:ARG:HG3	2.13	0.48
1:F:208:GLU:HG3	1:F:209:ARG:N	2.29	0.48
1:F:252:VAL:HA	1:F:260:ALA:HB2	1.94	0.48
1:F:143:LEU:CD2	1:F:372:LEU:HD22	2.43	0.48
1:B:417:GLY:HA2	1:B:420:GLN:OE1	2.14	0.48
1:C:252:VAL:HA	1:C:260:ALA:HB2	1.95	0.48
1:F:320:TRP:CD1	1:F:328:LEU:HD11	2.49	0.48
1:E:179:LEU:CD2	1:E:490:LEU:HD21	2.43	0.48
1:F:186:LEU:O	1:F:190:VAL:HG23	2.14	0.47
1:F:230:GLN:HA	1:F:248:ILE:O	2.14	0.47
1:A:26:ILE:HG22	1:A:53:LEU:CD1	2.43	0.47
1:D:238:MET:CE	1:D:295:HIS:CE1	2.98	0.47
1:C:60:ARG:HH22	1:E:56:LEU:HD21	1.78	0.47
1:E:417:GLY:HA2	1:E:420:GLN:OE1	2.14	0.47
1:E:86:MET:HE3	1:E:284:THR:HB	1.96	0.47
1:F:238:MET:CE	1:F:270:HIS:HB3	2.45	0.47
1:B:70:LEU:HB3	1:B:91:ARG:HG2	1.97	0.47
1:E:218:ILE:HA	1:E:221:TYR:HB2	1.97	0.47
1:D:136:GLU:CG	1:D:378:VAL:CG2	2.90	0.47
1:E:123:ARG:O	1:E:401:VAL:HG22	2.14	0.47
1:A:86:MET:HE3	1:A:285:PRO:HD2	1.97	0.47
1:A:111:HIS:CE1	1:A:137:LYS:HB3	2.50	0.47
1:E:286:LEU:HA	1:E:468:ARG:HB2	1.95	0.47
1:B:85:ARG:NH1	1:B:88:GLN:OE1	2.46	0.46
1:E:304:ASN:HB3	1:E:354:GLU:OE1	2.15	0.46
1:C:26:ILE:CG2	1:C:53:LEU:HD21	2.45	0.46
1:F:178:GLU:HG2	1:F:490:LEU:HD11	1.97	0.46
1:F:184:VAL:HB	1:F:185:PRO:HD3	1.97	0.46
1:A:474:GLU:O	1:A:478:ARG:HG3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:417:GLY:HA2	1:C:420:GLN:OE1	2.15	0.46
1:B:227:ARG:HD2	1:B:244:HIS:ND1	2.31	0.46
1:D:11:GLN:O	1:D:15:GLU:HG3	2.16	0.46
1:D:238:MET:HE2	1:D:270:HIS:HB3	1.99	0.45
1:E:9:GLN:HG3	1:E:10:TRP:N	2.31	0.45
1:F:428:LEU:HD21	1:F:484:LEU:HD13	1.98	0.45
1:B:366:GLU:HG2	1:B:369:ARG:NH2	2.31	0.45
1:F:502:GLY:O	1:F:503:VAL:O	2.35	0.45
1:B:53:LEU:HD12	1:B:53:LEU:HA	1.77	0.45
1:D:191:ILE:HD13	1:D:345:ARG:HG3	1.98	0.45
1:F:434:ALA:HA	1:F:437:GLU:HG2	1.99	0.45
1:F:502:GLY:O	1:F:503:VAL:HG22	2.15	0.45
1:C:9:GLN:N	4:C:709:HOH:O	2.50	0.45
1:D:56:LEU:O	1:D:60:ARG:HG2	2.17	0.45
1:E:184:VAL:HB	1:E:185:PRO:HD3	1.97	0.45
1:C:73:ALA:HA	1:C:76:ARG:HG3	1.98	0.45
1:B:338:ARG:HG2	1:B:500:LEU:CD2	2.46	0.45
1:B:473:GLY:O	1:B:477:GLU:HG3	2.16	0.45
1:F:53:LEU:HD23	1:F:53:LEU:HA	1.71	0.45
1:B:184:VAL:HB	1:B:185:PRO:HD3	1.99	0.45
1:E:103:GLU:OE1	1:E:106:ARG:NH2	2.50	0.45
1:E:219:ARG:HD3	4:E:708:HOH:O	2.16	0.45
1:B:36:THR:HG22	1:B:233:THR:CG2	2.47	0.44
1:C:60:ARG:HH22	1:E:56:LEU:CD2	2.29	0.44
1:E:252:VAL:HA	1:E:260:ALA:HB2	1.98	0.44
1:B:367:LEU:HG	4:B:799:HOH:O	2.17	0.44
1:D:252:VAL:HA	1:D:260:ALA:HB2	2.00	0.44
1:F:261:LEU:O	1:F:265:LEU:HG	2.18	0.44
1:F:314:ALA:HA	1:F:333:GLU:OE2	2.17	0.44
1:D:466:HIS:O	1:D:469:ARG:HB3	2.17	0.44
1:F:100:ILE:HD11	1:F:149:PHE:HE1	1.83	0.44
1:A:428:LEU:HD21	1:A:484:LEU:HD13	1.99	0.44
1:B:86:MET:HG2	1:B:286:LEU:HG	2.00	0.44
1:F:483:ALA:HB1	4:F:732:HOH:O	2.18	0.44
1:B:60:ARG:HH22	1:F:56:LEU:HD21	1.81	0.44
1:E:390:GLU:OE1	1:E:396:ARG:HD2	2.18	0.44
1:A:30:LEU:HD12	1:A:53:LEU:HD12	1.99	0.43
1:F:111:HIS:ND1	1:F:137:LYS:HD3	2.33	0.43
1:B:358:ASN:ND2	4:B:710:HOH:O	2.51	0.43
1:D:286:LEU:HA	1:D:468:ARG:HB2	1.99	0.43
1:B:427:VAL:HA	1:B:489:TYR:CG	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:428:LEU:HD21	1:C:484:LEU:HD13	2.00	0.43
1:C:261:LEU:O	1:C:265:LEU:HG	2.18	0.43
1:F:168:THR:O	1:F:172:VAL:HG23	2.18	0.43
1:F:364:ARG:HD3	1:F:419:PHE:CD1	2.53	0.43
1:F:305:LEU:HD13	1:F:433:TYR:CB	2.49	0.43
1:C:100:ILE:HD11	1:C:149:PHE:CE1	2.49	0.43
1:D:240:ARG:NH1	1:D:274:GLU:OE2	2.51	0.43
1:E:7:ASP:O	1:E:11:GLN:N	2.47	0.43
1:E:238:MET:HE2	1:E:270:HIS:HB3	2.00	0.43
1:A:123:ARG:O	1:A:401:VAL:HG22	2.19	0.43
1:D:103:GLU:HG2	1:D:104:PHE:N	2.34	0.43
1:E:460:ARG:HA	1:E:464:TYR:HB2	2.01	0.43
1:F:460:ARG:HA	1:F:464:TYR:HB2	1.99	0.43
1:B:56:LEU:HD21	1:F:60:ARG:HH21	1.83	0.43
1:D:26:ILE:HG22	1:D:53:LEU:CD1	2.49	0.43
1:E:209:ARG:NE	4:E:704:HOH:O	2.44	0.43
1:F:238:MET:HE2	1:F:270:HIS:HB3	1.99	0.42
1:E:191:ILE:HD13	1:E:345:ARG:HG3	2.00	0.42
1:C:337:TYR:CE2	1:C:500:LEU:HD21	2.54	0.42
1:E:489:TYR:CZ	1:E:493:LEU:HD11	2.54	0.42
1:A:238:MET:HE1	1:A:295:HIS:CE1	2.54	0.42
1:C:26:ILE:HG22	1:C:53:LEU:CD2	2.49	0.42
1:C:315:ALA:HB2	1:C:448:ALA:HA	2.00	0.42
1:F:238:MET:CE	1:F:295:HIS:CE1	3.02	0.42
1:C:90:ALA:HB2	1:C:285:PRO:HG2	2.02	0.42
1:E:390:GLU:HG2	1:E:396:ARG:HB2	2.00	0.42
1:A:460:ARG:HA	1:A:464:TYR:HB2	2.01	0.42
1:F:315:ALA:HB2	1:F:448:ALA:HA	2.01	0.42
1:B:19:GLU:OE1	1:B:60:ARG:NE	2.40	0.42
1:F:135:LEU:HB2	1:F:378:VAL:HG11	2.02	0.42
1:C:382:ALA:HB3	4:C:810:HOH:O	2.19	0.42
1:E:132:VAL:N	1:E:133:PRO:HD2	2.34	0.42
1:E:11:GLN:O	1:E:15:GLU:HG3	2.20	0.41
1:F:231:ASP:O	1:F:249:THR:HA	2.19	0.41
1:D:417:GLY:HA2	1:D:420:GLN:OE1	2.19	0.41
1:E:19:GLU:OE1	1:E:60:ARG:HD3	2.19	0.41
1:F:340:VAL:O	1:F:340:VAL:CG1	2.66	0.41
1:A:286:LEU:HA	1:A:468:ARG:HB2	2.00	0.41
1:C:427:VAL:HG13	1:C:486:ALA:HA	2.02	0.41
1:E:111:HIS:CE1	1:E:137:LYS:HD3	2.56	0.41
1:F:305:LEU:HD13	1:F:433:TYR:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:301:LEU:HD21	1:B:455:LEU:HD21	2.02	0.41
1:F:353:ASP:HB2	4:F:723:HOH:O	2.20	0.41
1:D:184:VAL:HB	1:D:185:PRO:HD3	2.02	0.41
1:F:132:VAL:N	1:F:133:PRO:HD2	2.35	0.41
1:B:23:PHE:CE2	1:B:60:ARG:HD3	2.55	0.41
1:A:252:VAL:HA	1:A:260:ALA:HB2	2.03	0.41
1:A:320:TRP:HE1	1:A:336:MET:HE3	1.86	0.41
1:C:9:GLN:N	4:C:712:HOH:O	2.54	0.41
1:D:241:LEU:N	1:D:241:LEU:HD12	2.35	0.41
1:F:364:ARG:HD3	1:F:419:PHE:CE1	2.56	0.41
1:A:65:GLY:O	1:A:69:LEU:CD1	2.69	0.41
1:A:305:LEU:HD13	1:A:433:TYR:HB2	2.03	0.41
1:E:9:GLN:OE1	1:E:76:ARG:HD2	2.20	0.41
1:F:30:LEU:CD1	1:F:53:LEU:HD12	2.51	0.41
1:F:314:ALA:HA	1:F:333:GLU:CD	2.41	0.41
1:A:96:LYS:HE2	1:A:96:LYS:HB3	1.92	0.40
1:C:279:ALA:HA	1:C:282:LEU:HG	2.04	0.40
1:D:460:ARG:HA	1:D:464:TYR:HB2	2.02	0.40
1:E:90:ALA:HB2	1:E:285:PRO:HG2	2.03	0.40
1:B:252:VAL:HA	1:B:260:ALA:HB2	2.02	0.40
1:F:111:HIS:CE1	1:F:137:LYS:HB3	2.55	0.40
1:A:334:GLU:OE1	1:A:338:ARG:NH1	2.53	0.40
1:B:427:VAL:HG22	1:B:428:LEU:N	2.36	0.40
1:E:111:HIS:ND1	1:E:137:LYS:HD3	2.36	0.40
1:E:156:LEU:CD2	1:E:369:ARG:HG3	2.52	0.40
1:A:65:GLY:O	1:A:69:LEU:HD13	2.22	0.40
1:D:90:ALA:HB2	1:D:285:PRO:HG2	2.03	0.40
1:E:111:HIS:CE1	1:E:137:LYS:HB3	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	495/503 (98%)	488 (99%)	7 (1%)	0	100	100
1	B	500/503 (99%)	491 (98%)	9 (2%)	0	100	100
1	C	493/503 (98%)	487 (99%)	6 (1%)	0	100	100
1	D	495/503 (98%)	489 (99%)	6 (1%)	0	100	100
1	E	495/503 (98%)	487 (98%)	8 (2%)	0	100	100
1	F	499/503 (99%)	491 (98%)	8 (2%)	0	100	100
All	All	2977/3018 (99%)	2933 (98%)	44 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	380/392 (97%)	375 (99%)	5 (1%)	69	84
1	B	388/392 (99%)	382 (98%)	6 (2%)	65	80
1	C	384/392 (98%)	379 (99%)	5 (1%)	69	84
1	D	383/392 (98%)	379 (99%)	4 (1%)	76	88
1	E	380/392 (97%)	372 (98%)	8 (2%)	53	72
1	F	384/392 (98%)	380 (99%)	4 (1%)	76	88
All	All	2299/2352 (98%)	2267 (99%)	32 (1%)	69	82

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	103	GLU
1	A	108	PHE
1	A	259	ASP
1	A	273	TYR
1	A	295	HIS
1	B	108	PHE
1	B	151	GLU

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Mol	Chain	Res	Type
1	B	238	MET
1	B	259[A]	ASP
1	B	259[B]	ASP
1	B	295	HIS
1	C	108	PHE
1	C	295	HIS
1	C	340	VAL
1	C	460	ARG
1	C	485	THR
1	D	14	THR
1	D	108	PHE
1	D	295	HIS
1	D	460	ARG
1	E	108	PHE
1	E	167	MET
1	E	259	ASP
1	E	273	TYR
1	E	295	HIS
1	E	310	ARG
1	E	340	VAL
1	E	456	HIS
1	F	108	PHE
1	F	259	ASP
1	F	273	TYR
1	F	295	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 7 ligands modelled in this entry, 6 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	ACT	D	602	2	3,3,3	0.73	0	3,3,3	1.46	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	602	ACT	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	497/503 (98%)	-0.39	0	100	100	17, 24, 45, 66	0
1	B	501/503 (99%)	-0.34	1 (0%)	95	94	18, 24, 42, 64	0
1	C	495/503 (98%)	-0.26	2 (0%)	92	91	20, 28, 42, 65	0
1	D	497/503 (98%)	-0.25	6 (1%)	79	77	18, 25, 45, 65	0
1	E	497/503 (98%)	-0.14	6 (1%)	79	77	21, 35, 57, 78	0
1	F	501/503 (99%)	-0.08	3 (0%)	89	88	19, 34, 52, 64	0
All	All	2988/3018 (99%)	-0.24	18 (0%)	89	88	17, 28, 49, 78	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	9	GLN	3.3
1	F	11	GLN	3.0
1	E	12	GLN	2.7
1	E	11	GLN	2.5
1	D	77	SER	2.4
1	E	114	GLN	2.4
1	D	79	LEU	2.3
1	E	72	ALA	2.3
1	E	80	SER	2.3
1	D	321	ARG	2.3
1	F	497	TYR	2.2
1	C	234	HIS	2.1
1	D	72	ALA	2.1
1	B	114	GLN	2.1
1	D	64	ALA	2.1
1	C	11	GLN	2.1
1	F	183	LEU	2.0
1	D	234	HIS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	ACT	D	602	4/4	0.89	0.17	20,20,32,32	0
2	ZN	B	601	1/1	0.99	0.12	25,25,25,25	0
2	ZN	D	601	1/1	0.99	0.14	25,25,25,25	0
2	ZN	E	601	1/1	0.99	0.13	33,33,33,33	0
2	ZN	F	601	1/1	0.99	0.13	30,30,30,30	0
2	ZN	A	601	1/1	0.99	0.13	24,24,24,24	0
2	ZN	C	601	1/1	1.00	0.15	32,32,32,32	0

6.5 Other polymers (i)

There are no such residues in this entry.